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EXAMINER
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BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

Paper No. 16

Application Number: 09/747,804
Filing Date: December 22, 2000
Appellant(s): HILLMAN ET AL.

Lori L. Kerber and Michelle M. Stempien
For Appellant

EXAMINER'S ANSWER

This is in response to the appeal brief filed 7/3/2003.

(1) Real Party in Interest

A statement identifying the real party in interest is contained in the brief.

(2) Related Appeals and Interferences

A statement identifying the related appeals and interferences which will directly affect or be directly affected by or have a bearing on the decision in the pending appeal is contained in the brief.

(3) Status of Claims

The statement of the status of the claims contained in the brief is correct.

(4) Status of Amendments After Final

The appellant's statement of the status of amendments after final rejection contained in the brief is correct.

(5) Summary of Invention

The summary of invention contained in the brief is correct.

(6) Issues

The appellant's statement of the issues in the brief is correct with regards to whether claims 1 and 13 directed to EXADH polypeptide sequences meet the written description requirement of 35 USC 112, first paragraph.

(7) Grouping of Claims

The appellant's statement in the brief that claims stand or fall together is correct.

(8) Claims Appealed

The copy of the appealed claims contained in the Appendix to the brief is correct.

(9) Prior Art of Record

No prior art is relied upon by the examiner in the rejection of the claims under appeal.

(10) Grounds of Rejection

The following ground(s) of rejection are applicable to the appealed claims:

Claims 1 and 13 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 1 and 13 are directed to all possible polypeptides selected from the group consisting of: a) any polypeptide comprising an amino acid sequence of SEQ ID NO: 1, b) any polypeptide comprising a naturally-occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 1, said naturally occurring amino acid sequence having extracellular adhesion activity (claim 1), and compositions comprising said polypeptide and an excipient (claim 13). The specification, however, only provides the representative species of SEQ ID NO: 1, encompassed by these claims. There is no disclosure of any particular structure to function/activity relationship for the disclosed species. Specifically part b) of claim 1 is drawn to all possible polypeptides comprising a naturally-occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 1, said naturally occurring amino acid sequence having extracellular adhesion activity. This encompasses allelic variants of SEQ ID NO: 1.

The specification defines an "allelic sequence" (see page 7) as an alternative form of the gene which may result in at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. This definition does not provide any specific information about the structure of naturally occurring (alleles) variants of SEQ ID NO: 1 (i.e. where are the regions within which mutations are likely to occur) nor discloses any function for naturally occurring variants. There is no description of the mutational sites that exist in nature, and there is no description of how the structure of SEQ ID NO: 1 relates to the structure of any naturally occurring alleles. The general knowledge in the art concerning alleles does not provide any indication of how one allele is representative of unknown alleles. The nature of alleles is such that they are variant structures, and in the present state of the art, the structure of one does not provide guidance to the structure of others.

The genus of proteins that are claimed is a large variable genus. The specification also fails to describe additional representative species of these polypeptides by any identifying characteristics or properties other than the structural characteristics recited in claim 1, for which no predictability of function is apparent. Since the claimed genus encompasses polypeptides yet to be discovered, fusion proteins, etc., the disclosed structural feature of SEQ ID NO: 1 does not "constitute a substantial portion" of the claimed genus. Given this lack of additional representative species as encompassed by the claims, applicants have failed to sufficiently describe

the claimed invention, in such full, clear, concise, and exact terms that a skilled artisan would recognize applicants were in possession of the claimed invention.

Appellant is referred to the revised guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at www.uspto.gov.

(11) Response to Argument

Appellants submit that the specification provides an adequate written description of the claimed "variants" of SEQ ID NO: 1. Appellants argue that SEQ ID NO: 1 is specifically disclosed in the application and that polypeptide variants having at least 90% identity to SEQ ID NO: 1 are described at for example page 14, lines 8-11. It is noted that the description to which appellants refer to at page 14, lines 8-11 consists of the general description of the metes and bounds of the claimed genus (i.e. "The invention also encompasses EXADH variants...about 95% amino acid sequence identity to the EXADH amino acid sequence) and not the actual description of a single member of the claimed genus. Appellants argue that one of ordinary skill in the art would recognize polypeptide sequences which are variants at least 90% identical to SEQ ID NO: 1 and that given any naturally occurring polypeptide sequence, it would be routine for one of skill in the art to recognize whether it was a variant of SEQ ID NO: 1. Herein lies appellants' problem. Appellants argue that "given a naturally occurring polypeptide sequence", one would be able to recognize whether it was a variant of SEQ ID NO: 1. Appellants have only "given one naturally occurring polypeptide sequence", that comprising the amino acid sequence of SEQ ID NO: 1. Appellants argument is not

found persuasive because the question is not whether one would be able to determine whether a given naturally occurring polypeptide is a variant of SEQ ID NO: 1, but rather have appellants described said naturally occurring polypeptides sufficiently that one of skill in the art would recognize that appellant was in possession of said naturally occurring polypeptide variants of SEQ ID NO: 1. As stated previously and above appellants have merely described a single naturally occurring polypeptide (i.e. that polypeptide comprising the amino acid sequence of SEQ ID NO: 1).

Appellants further argue that claim 1 recites not only that the polypeptide "variants" have extracellular adhesion activity as well as having at least 90% sequence identity to SEQ ID NO: 1, but also "have a naturally occurring amino acid sequence" and that given the information provided by SEQ ID NO: 1 (the amino acid sequence of EXADH-1) and SEQ ID NO: 3 (the polynucleotide sequence encoding EXADH-1) one of skill would be able to routinely obtain "a naturally occurring amino acid sequence having extracellular adhesion activity" as recited in claim 1. Appellant is reminded that the rejection at issue is not one of enablement and the question at issue is not whether one of skill in the art would be able to "obtain" a "naturally occurring amino acid sequence having extracellular adhesion activity", but rather given the lack of representative species as encompassed by the claims, described by appellants, appellants have failed to sufficiently describe the claimed invention, in such full, clear, concise, and exact terms that a skilled artisan would recognize appellants were in possession of the claimed invention.

Appellants argue that the present claims specifically define the claimed genus through the recitation of chemical structure based on the relationship to SEQ ID NO: 1, however appellants do not define in any way the claimed genus of those "naturally occurring amino acid sequences" with the claimed chemical structure.

The examiner fully acknowledges appellants' recitation of the structural limitations of the polypeptides of claim 1 part b) and appellants' attempts to claim polypeptides based solely on the structural definitions as recited in claim 1 part b). However, the polypeptides as defined in claim 1 part b) encompass a genus of polypeptides that encompasses widely variant species. While one of skill in the art, provided the sequence of SEQ ID NO:1, may be able to recognize variants of SEQ ID NO:1 with an amino acid sequence sharing greater than 90 % identity, one cannot recognize which of these variants occurs naturally and is thus encompassed by the genus of claim 1 part b). Therefore, the skilled artisan would not be able to envision all of the members of the claimed genus of polypeptides merely from its structural limitations. The single disclosed polypeptide comprising the amino acid sequence of SEQ ID NO:1 is not representative of the entire genus of thus claimed naturally occurring polypeptides and one of skill in the art would *not* recognize that appellants were in possession of all polypeptides comprising a naturally-occurring amino acid sequence at least 90% identical to SEQ ID NO:1.

Appellants argue that the present claims do not define a genus which is "highly variant" and present the reference Brenner et al. (PNAS Vol 95: 6073-6078, 1998) in support of this position. Appellants submit that Brenner et al. have determined that 30%

identity is a reliable threshold for establishing evolutionary homology between two sequences aligned over at least 150 residues. Appellants argue that therefore "naturally occurring molecules" may exist which could be characterized as human prostate carcinoma tumor antigen-1 or galectin proteins and which have as little as 30% identity over a region of at least 150 residues of SEQ ID NO: 1. While it may be that an evolutionary relationship may exist between two molecules with as little as 30% identity over a region of at least 150 residues, this does not in any way reflect on the description of those naturally occurring molecules or whether a single species is representative of the claimed naturally occurring molecules.

Appellants further argue that the state of the art at the time of the present invention is further advanced than at the time of the *Lilly* and *Fiers* applications and the written description decisions based on these cases. Appellants submit that based on the developments in the field of recombinant DNA technology since these decisions (i.e. the "dark ages" of recombinant DNA technology), one of skill in the art would recognize that given the sequence information of SEQ ID NO: 1 and the additional extensive detail provided by the subject application, the present inventors were in possession of the claimed polypeptide variants. These arguments are not found persuasive. Appellants argument again appears to be directed towards whether one of skill in the art would be able to "obtain" a "naturally occurring amino acid sequence having extracellular adhesion activity", Appellants argument does not help appellants in their rebuttal that given the lack of representative species as encompassed by the claims, appellants have failed to sufficiently describe the claimed invention, in such full, clear, concise, and

exact terms that a skilled artisan would recognize appellants were in possession of the claimed invention.

Appellants further argue that the examiner has attempted to apply a standard for written description different from that which is required by law.

The Court of Appeals for the Federal Circuit has recently held that a "written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as be structure, formula [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." University of California v. Eli Lilly and Co., 1997 U.S. App. LEXIS 18221, at *23, quoting Fiers v. Revel, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993) (bracketed material in original). To fully describe a genus of genetic material, which is a chemical compound, applicants must (1) fully describe at least one species of the claimed genus sufficient to represent said genus whereby a skilled artisan, in view of the prior art, could predict the structure of other species encompassed by the claimed genus and (2) identify the common characteristics of the claimed molecules, e.g., structure, physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or a combination of these.

In the instant specification, a single polypeptide comprising SEQ ID NO: 1 is fully described in the form of SEQ ID NO:1, wherein the polypeptide has extracellular adhesion activity. This is but a single species of the claimed genus. Those sequences that are "naturally occurring" are a subset of the genus having 90% identity to instantly disclosed SEQ ID NO: 1. The specification does not adequately describe this subset

according to its structure so that one of skill in the art would be able to predict naturally occurring sequences, particularly in view of the larger genus that includes both naturally and "manufactured" sequences. Therefore, the instant claims are not adequately described.

For the above reasons, it is believed that the rejections should be sustained.

Respectfully submitted,

Richard G. Hutson, Ph.D.
September 22, 2003

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